

10/561092

034123-109\_ST25.txt  
SEQUENCE LISTING  
PCT/PTO 16 DEC 2005

<110> THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
DOWDY, Steven F  
WADIA, Jehangir S

<120> POLYPEPTIDE TRANSDUCTION AND FUSOGENIC PEPTIDES

<130> 034123-109

<140> PCT/US2004/20837  
<141> 2004-06-18

<150> 60/480,065  
<151> 2003-06-20

<160> 21

<170> PatentIn version 3.3

<210> 1  
<211> 86  
<212> PRT  
<213> Unknown

<220>  
<223> transducing protein

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Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly  
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
50 55 60

His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Arg Gly Asp  
65 70 75 80

Pro Thr Gly Pro Lys Glu  
85

<210> 2  
<211> 20  
<212> PRT  
<213> Unknown

<220>  
<223> HA2 analog

<400> 2

Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Thr Gly  
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Met Ile Asp Gly  
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<210> 3  
<211> 20  
<212> PRT  
<213> Unknown

<220>  
<223> HA2 analog

<400> 3

Gly Leu Phe Glu Ala Ile Ala Glu Phe Ile Glu Gly Gly Trp Glu Gly  
1 5 10 15

Leu Ile Glu Gly  
20

<210> 4  
<211> 5  
<212> PRT  
<213> Unknown

<220>  
<223> linker moiety

<400> 4

Gly Gly Gly Gly Ser  
1 5

<210> 5  
<211> 6  
<212> PRT  
<213> Unknown

<220>  
<223> linker moiety

<220>  
<221> Xaa  
<222> (6)..(6)  
<223> Xaa = any number of repeats of amino acids 1-5

<400> 5

Gly Gly Gly Gly Ser Xaa  
1 5

<210> 6  
<211> 12

<212> PRT  
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<220>  
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<400> 6

Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser  
 1 5 10

<210> 7  
 <211> 14  
 <212> PRT  
 <213> Unknown

<220>  
 <223> linker moiety

<400> 7

Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly  
 1 5 10

<210> 8  
 <211> 18  
 <212> PRT  
 <213> Unknown

<220>  
 <223> linker moiety

<400> 8

Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Ser Gly Ser Thr  
 1 5 10 15

Lys Gly

<210> 9  
 <211> 18  
 <212> PRT  
 <213> Unknown

<220>  
 <223> linker moiety

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Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr  
 1 5 10 15

Lys Gly

<210> 10

<211> 14  
 <212> PRT  
 <213> Unknown

<220>  
 <223> linker moiety

<400> 10

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Glu Phe  
 1 5 10

<210> 11  
 <211> 30  
 <212> PRT  
 <213> Unknown

<220>  
 <223> HA2 TAT peptide

<400> 11

Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly  
 1 5 10 15

Met Ile Asp Gly Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
 20 25 30

<210> 12  
 <211> 20  
 <212> PRT  
 <213> Unknown

<220>  
 <223> HA2 peptide

<400> 12

Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly  
 1 5 10 15

Met Ile Asp Gly  
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<210> 13  
 <211> 418  
 <212> DNA  
 <213> Unknown

<220>  
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 atgggcagca gccatcatca tcatcatcac agcagcggcc tggcgccgcg cggcagccat 180  
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atgaggaaga agcggagaca gcgacgaaga ggctcggatc cgaattcgag ctccgtcgac	240
aagcttgcgg ccgcactcga gcaccaccac caccaccact gagatccggc tgctaacaaa	300
gcccgaaggg aagctgagtt ggctgctgcc accgctgagc aataactagc ataaccctt	360
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tactccttct tcgcctctgt cgctgcttct ccgagcctag gcttaagctc gaggcagctg	240
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 <211> 53  
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<220>  
 <223> TAT peptide

<400> 15

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1 5 10 15

Arg Gly Ser His Met Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Ser
20 25 30

Asp Pro Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu Glu His
35 40 45

His His His His His
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<210> 16  
 <211> 360  
 <212> DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; cDNA

&lt;400&gt; 16

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atgggcagga agaagcggag acagcgacga agaggccata tggctagcat gactggtgga      180
cagcaaattg gtcgggatcc gaattcgagc tccgtcgaca agcttgcggc cgcactcgag      240
caccaccacc accaccactg agatccggct gctaacaaag cccgaaagga agctgagttg      300
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&lt;210&gt; 17

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; cDNA

&lt;400&gt; 17

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taccgcctct tcttcgcctc tgctcgctgct tctccggtat accgatcgta ctgaccacct      180
gtcgtttacc cagccctagg cttaagctcg aggcagctgt tcgaacgccg gcgtgagctc      240
gtggtggtgg tgggtggtgac tctaggccga cgattgtttc gggctttcct tcgactcaac      300
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&lt;210&gt; 18

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; TAT peptide

&lt;400&gt; 18

```

Met Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly His Met Ala Ser
1           5           10           15

```

```

Met Thr Gly Gly Gln Gln Met Gly Arg Asp Pro Asn Ser Ser Ser Val
          20           25           30

```

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Asp Lys Leu Ala Ala Ala Leu Glu His His His His His His
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 agaggccata tggctagcat gactggtgga cagcaaatgg gtcgggatcc gaattccatg 240  
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 gaggttcgca agaacctgat ggacatgttc agggatcgcc aggcgttttc tgagcatacc 360  
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 aaatggtttc ccgcagaacc tgaagatgtt cgcgattatc ttctatatct tcaggcgcgc 480  
 ggtctggcag taaaaactat ccagcaacat ttgggcccagc taaacatgct tcatcgctcg 540  
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&lt;220&gt;

&lt;223&gt; cDNA

&lt;400&gt; 20

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aaaacaaatt gaaattcttc ctctatatgg taccgcctct tcttcgcctc tgtcgctgct    180
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&lt;210&gt; 21

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; TAT peptide

&lt;400&gt; 21



## 034123-109.ST25.txt

Met Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly His Met Ala Ser  
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 Met Thr Gly Gly Gln Gln Met Gly Arg Asp Pro Asn Ser Met Ser Asn  
 20 25 30  
 Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val Asp Ala Thr  
 35 40 45  
 Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg Asp Arg Gln  
 50 55 60  
 Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val Cys Arg Ser  
 65 70 75 80  
 Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu  
 85 90 95  
 Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu  
 100 105 110  
 Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn Met Leu His  
 115 120 125  
 Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala Val Ser Leu  
 130 135 140  
 Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly Glu Arg Ala  
 145 150 155 160  
 Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln Val Arg Ser  
 165 170 175  
 Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe  
 180 185 190  
 Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg  
 195 200 205  
 Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg Met Leu Ile  
 210 215 220  
 His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly Val Glu Lys  
 225 230 235 240  
 Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp Ile Ser Val  
 245 250 255

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Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg  
260 265 270

Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg  
275 280 285

Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile Tyr Gly Ala  
290 295 300

Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly His Ser Ala  
305 310 315 320

Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val Ser Ile Pro  
325 330 335

Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile Val Met Asn  
340 345 350

Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu  
355 360 365

Glu Asp Gly Asp Ala Ala Ala Leu Glu His His His His His His  
370 375 380